REMARKS

The specification has been amended to correct inadvertent typographical and grammatical errors and the claims have been amended to clarify the invention. In particular, the specification has been amended at the paragraph beginning at line 35 of page 12 to recite cDNAs having "about 88% to about 96% sequence identity to the cDNA encoding the human protein ---". Claim 1 has been amended at element b) to recite an amino acid sequence having "at least 95% sequence identity to SEQ ID NO:4". Support for the amendment to claim 1 is found in the specification, for example, at p. 11, lines 13-19 which describes variants of the amino acid and nucleotide sequences of the invention. No new matter is added by these amendments, and entry of the amendment is respectfully requested..

Restriction Requirement

In the Restriction Requirement, the Examiner requested Applicants to elect one of the following inventions:

Group I (claims 1-4) drawn to purified proteins, antigenic epitopes thereof, or biologically active portions thereof.

Group II (claims 5-6) drawn to a method of screening a plurality of compounds to identify ligands.

Group III (claims 7-8 and 10-11) drawn to isolated polyclonal or monoclonal antibodies and methods of making such.

Group IV (claim 9) drawn to an agonist.

Group V (claims 12-15) drawn to a method of using polyclonal or monoclonal antibodies to detect expression of a polypeptide.

The Examiner further started that claim 6 is generic to a plurality of disclosed patentably distinct species and further required an election of a single species for prosecution on merits selected from; a) DNA molecules and RNA molecules, b) peptide nucleic acids, c) peptides, proteins, and mimetics, d) agonists, e) antagonists, f) antibodies, immunoglobulins, inhibitors, and g) drugs.

Applicants hereby elect, with traverse, to prosecute Group I, which includes and is drawn to Claims 1-4 . Applicants submit that the claims of Group I could be examined together with their methods of use, Group II (claims 5-6), as well as with claims drawn to antibodies specific for the polypeptides of Group I, Group III (claims 7-8 and 10-11), as well as their methods of use, Group V (claims 12-15), without undue burden. Antibodies to detect the polypeptides of the invention would be

found in a search for the novelty of the polypeptides themselves, as well as methods of use of the polypeptides and antibodies specific for them that are limited in scope to the compositions of matter. Applicants further object to the election of species requirement for the potential ligands recited in claim 6 as the subject matter of the claim is a method of use of the polypeptides of claim 1 and not to the potential ligands themselves. Applicants therefore request reconsideration and withdrawal of the Restriction Requirement and examination of claims 1-8 and 10-15. In the event the Examiner maintains the Restriction Requirement, Applicants submit that claims 5-8 are methods of use of the polypeptides of claim 1 that depend from and are of the same scope as claim 1 and are therefore subject to rejoinder pending allowance of claim 1 in accordance with *In re Ochiai and Brouwer* and the MPEP § 1801.04.

Applicants reserve the right to prosecute the subject matter of non-elected claims in subsequent divisional applications.

Applicants believe that no fee is due with this communication. However, if the USPTO determines that a fee is due, the Commissioner is hereby authorized to charge Deposit Account No. 09-0108.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

Paragraph(s) beginning at line 35of page 12 has been amended as follows:

cDNAs encoding the tumor suppressor were identified using BLAST2 with default parameters and the ZOOSEQ databases (Incyte Genomics, Palo Alto CA). These cDNAs have from about 88% to about 96% [amino acid] sequence identity to the cDNA encoding the human protein as shown in the table below. The first column shows the SEQ ID_H for the human cDNA; the second column, the SEQ ID_{FR} for fragment cDNAs; the third column, the sequence numbers for the fragments; the fourth column, the species; the fifth column, percent identity to the human cDNA; and the sixth column, the nucleotide alignment (Nt_H) of the human and variant cDNAs.

IN THE CLAIMS:

Claim 1 has been amended as follows:

1. (Once Amended) A purified protein comprising an amino acid sequence selected from the group consisting of:

a) an amino acid sequence of SEQ ID NO:4; and

b) an amino acid sequence having at least 95[83]% sequence identity to SEQ ID NO:4.